

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:43:18 ; Search time 27.9564 seconds
(without alignments)
1237.942 Million cell updates/sec

Title: US-09-625-573-4
Perfect score: 1000
Sequence: 1 MLSTSRFRIRNTNESGEV.....DGVSTNTPTSGEVSAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1900	100.0	360	2 JC2443	chemokine (C-C) re
2	1651.5	86.9	374	2 I38450	chemokine (C-C) re
3	1364	71.8	352	2 A43113	chemokine (C-C) re
4	1036	54.5	355	2 A45177	chemokine (C-C) re
5	1010.5	53.2	359	2 I49341	Mip-1 alpha recept
6	963.5	50.7	355	2 I49339	macrophage inflamm
7	951	50.1	355	2 G02436	chemokine (C-C) re
8	871	45.8	360	2 JC4587	chemokine (C-C) re
9	862.5	45.4	360	2 A57160	chemokine (C-C) re
10	822.5	43.3	383	2 S55594	G protein-coupled
11	778.5	41.0	356	2 I49340	Mip-1 alpha recept
12	751	39.5	355	2 JC5067	G protein-coupled
13	722.5	38.0	354	2 I58186	Probable G protein
14	708	37.3	355	2 JC4304	orphan G protein-c
15	649.5	34.2	344	2 JC5942	chemokine receptor
16	581.5	30.6	378	2 B55735	lymphocyte-specifi
17	569	29.9	378	2 A55735	G protein-coupled
18	567.5	29.9	378	2 A45680	G protein-coupled
19	563	29.6	369	2 JC5068	G protein-coupled
20	547	28.8	360	2 A53611	interleukin-8 rece
21	540.5	28.4	355	2 JQ1231	interleukin-8 rece
22	540.5	28.4	359	2 A48921	interleukin-8 rece
23	536.5	28.2	358	2 A53752	interleukin-8 rece
24	532.5	28.0	356	2 S42096	interleukin-8 rece
25	532	28.0	367	2 JF0349	interferon-inducib
26	528.5	27.8	333	2 I65989	G protein-coupled
27	528.5	27.8	350	2 A39445	interleukin-8 rece
28	515.5	27.1	352	2 G00048	fusin (LESTRA) - c
29	515	27.1	353	2 S28787	neuropeptide Y/pep

ALIGNMENTS

RESULT 1
JC2443

chemokine (C-C) receptor 2, splice form B - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C:Accession: JC2443; I38463

R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant
A:Reference number: JC2443; MUID:94324942; PMID:8048929
A:Accession: JC2443
A:Molecule type: mRNA
A:Residues: 1-360 <I>AM>
A:Cross-references: DDBJ:D29984; NID:9531246; PIDN:BAA06253.1; PID:9531247
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U03905; NID:9472557; PIDN:AAA19120.1; PID:9472558
C:Genetics:
A:Gene: GDB:CMKBR2
A:Map position: 3p21-3p21
A:Cross-references: GDB:337364; OMIM:601267
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein; transmembrane #status predicted <TM1>
F:81-100/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:207-226/Domain: transmembrane #status predicted <TM5>
F:244-268/Domain: transmembrane #status predicted <TM6>
F:287-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1900; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.2e-154;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTFDDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60
|||||

Db 1 MLSTSRFRIRNTNESGEVTFDDYDYGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60
|||||

QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLLITLPLWAHSAANEWFGNCKLFTGLY 120
|||||

Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLLLITLPLWAHSAANEWFGNCKLFTGLY 120
|||||

QY 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
QY 181 COKEDSVVCGPYFPGWNNFTHIRNIGLVLPPLIMWICYSGLKTLRCRNEKKRRH 240
Db 181 COKEDSVVCGPYFPGWNNFTHIRNIGLVLPPLIMWICYSGLKTLRCRNEKKRRH 240
QY 241 AVRVIITIMVYFLEWTPYINIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIITIMVYFLEWTPYINIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVFYRETVGVTSNTSTGTGQEVSA 360
Db 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVFYRETVGVTSNTSTGTGQEVSA 360
RESULT 2
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>
A;Cross-references: EMBL:003882; NID:9472555; PIDN:AAA19119.1; PID:g472556
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted
Query Match 86.9%; Score 1651.5; DB 2; Length 374;
Best Local Similarity 95.5%; Pred. No. 5.9e-133;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
QY 1 MLSTSRFRINTNSESGETVTFDDYDYGAPCHKFDVKQIGALLPPLSLVFIFFGVGN 60
Db 1 MLSTSRFRINTNSESGETVTFDDYDYGAPCHKFDVKQIGALLPPLSLVFIFFGVGN 60
QY 61 MLVVLILNCKKLCTDIYLLNLAISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120
Db 61 MLVVLILNCKKLCTDIYLLNLAISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120
QY 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
QY 181 COKEDSVVCGPYFPGWNNFTHIRNIGLVLPPLIMWICYSGLKTLRCRNEKKRRH 240
Db 181 COKEDSVVCGPYFPGWNNFTHIRNIGLVLPPLIMWICYSGLKTLRCRNEKKRRH 240
QY 241 AVRVIITIMVYFLEWTPYINIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIITIMVYFLEWTPYINIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300

QY 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPV 334
Db 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPV 334
RESULT 3
A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sazag
M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184; 'INDSHLGAGPAAACHGHLILGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:gl524062; PIDN:CAA67767.1; PID:gl524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a
nd may have had a selective advantage by conferring resistance to Yersinia plague inf
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:gl502408; PIDN:AAH17071.1; PID:gl502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemok
A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:gl457945; PIDN:AAH50598.1; PID:gl457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (A
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and R
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmem
F:32-56/Domain: transmembrane #status predicted <TM1>

F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;142-166/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM6>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 71.8%; Score 1364; DB 2; Length 352;
Best Local Similarity 75.5%; Pred. No. 1.6e-108;
Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYD--GAPCHKFDVKGQIAQLLPPLYSLVFIFGFGNMLVLLINCKKLCITDYL 81
Db 10 YDNIYTSPPCQKLNKQIAARLLPPLYSLVFIFGFGNMLVLLINCKKLSMTDYL 69

QY 82 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIILLTIDRYLA 141
Db 70 LNLAISSLFELLVFPWAHAAQWDFGNTMCQLLTGLYFIFGFGFIILLTIDRYLA 129

QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVCGPYPP---RG 197
Db 130 VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIITRQKEGLHYTCSSHPFPYQYF 189

QY 198 WNNFHTIMRNILGLVPLLMVVCYSGLKTLRCRNEKRRHRAVRVIFTIMIVYFLWT 257
Db 190 WKNFQTLKIVILGLVPLLMVVCYSGLKTLRCRNEKRRHRAVRVIFTIMIVYFLWA 249

QY 258 PYNIVLLNTFQFFGLSNCESTSQLDAQVTETLGMTHCCINPIIYAFVGEKFRYLS 317
Db 250 PYNIVLLNTFQFFGLSNCESTSQLDAQVTETLGMTHCCINPIIYAFVGEKFRNLL 309

QY 318 VFRKHKTKRCKOCVPVYRETVDGVTSTNTPSPGGEVSAGL 360
Db 310 VFFQKHAKRCKCCSIFQGEAPERASSVYTRSTGEGEISVGL 352

RESULT 4
A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-
C chemokine receptor, human macrophage inflammatory protein-1 (MIP-1)
A;Reference number: A45177; MUID:93161416; PMID:7679328
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr

F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-98/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 54.5%; Score 1036; DB 2; Length 355;
Best Local Similarity 56.4%; Pred. No. 1.2e-80;
Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

QY 12 NTNSESSEVTFDFDYCAPCHKFDVKGQIAQLLPPLYSLVFIFGFGNMLVLLINCK 71
Db 5 NTTED-VDTTFDFDYCAPCHKFDVKGQIAQLLPPLYSLVFIFGFGNMLVLLVLYOK 63

QY 72 KKLCTDIYLLNLAISSDLLFLITPLMA-HSAANEWFGNAMCKLFTGLYHIGYFGGFI 130
Db 64 RLKNTSIYLLNLAISSDLLFLITPLFWIDYKLDKDDWFGDAMCKLISGFIYTGLEYSEIFF 123

QY 131 IILITIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVVC 190
Db 124 IILITIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVVC 183

QY 191 GPYPP---RGNNFHTIMRNILGLVPLLMVVCYSGLKTLRCRNEKRRHRAVRVIF 246
Db 184 SLHPEHSLREKWLFOALKNLGLVPLLMVVCYSGLKTLRCRNEKRRHRAVRVIF 242

QY 247 TIMVYFLFWPYNIVLLNTFQFFGLSNCESTSQLDAQVTETLGMTHCCINPIIYA 306
Db 243 VIMIIFLFWPYNIVLLNTFQFFGLSNCESTSQLDAQVTETLGMTHCCINPIIYA 302

QY 307 FVGEKFRYLSVFRKHKTKRCKOCVPVYRETVDGVTSTNTPSPGGEVSAGL 359
Db 303 FVGERFRKYLQFLHRRVAVHLVKWLPLSVDRLERSVST-SPSTGEHLSAG 354

RESULT 5
I49341
MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
receptor-like-2 (MIP-1L2) cDNAs
A;Reference number: I49341; MUID:95340546; PMID:7542241
A;Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

Query Match 53.2%; Score 1010.5; DB 2; Length 359;
Best Local Similarity 53.5%; Pred. No. 1.9e-78;
Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

QY 10 IRNTNESSEVTFDFDYCAPCHKFDVKGQIAQLLPPLYSLVFIFGFGNMLVLLIN 69
Db 8 IKTVVESE--TTPYEWEAPCEKVRKELGSLWLLPPLYSLVFIFGLGNMNVLLIK 65

QY 70 CKKLKCLFDIYLLNLAISSDLLFLITPLMAHSA--NEWFGNAMCKLFTGLYHIGYFGGI 128
Db 66 YRKLQIMTNIVLNLAISSDLLFLITVPEWVHVLNNEWFGHGMCKMLSGFYLYALYSEI 125

QY 129 FFIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVY 188
Db 126 FFIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVY 185

QY 189 VCGPFPFRG-----WNNFHTIMRNILGLVPLLLIMVICYSIGILKTLRCRNEKKRHRVAVR 244
 Db 186 SCSRYPEGEEDSWKRFHMRNIFGLALPLLVWVICYSIGIIKTLRCPN-KKKHKAIRL 244
 QY 245 IFTIMIVYFLWTPYNNIVILLNTFQEFFGLSNCESISOLDQATQVITLGMTCCINPIL 304
 Db 245 IFVWMLVFFIFWTPYNNIVLLFSAFHSFTELECEQSKHLDLQWQVTEVIATHTCCVNPVI 304
 QY 305 YAFVGEKFRYLSVFRKHKTRCKCPVYFRET-----DGVTSNTSTPSTGQEV 356
 Db 305 YAFVGERFRKHLRLEFHRNVQ-----FTWENIFQPLPGENGRTSSVSTGQEI 355
 QY 357 S 357
 Db 356 S 356

RESULT 6

I49339

crophage inflammatory protein-1 alpha receptor - mouse

Species: Mus musculus (house mouse)

Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I49339

R:Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine

A:Reference number: I49339; MUID:95340546; PMID:7542241

A:Accession: I49339

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <RES>

A:Cross-references: EMBL:U28404; NID:g981547; PIDN:AAA89153.1; PID:g801548

C:Superfamily: vertebrate rhodopsin

Query Match 50.7%; Score 963.5; DB 2; Length 355;
 Best Local Similarity 52.3%; Pred. No. 1.8e-74;
 Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;

QY 21 TTFEDYDYGAPCHKEDVKQIGAOQLPPLYSILVIFGFGVGNMLVLLINCKKLCLTDIY 80
 Db 13 TTEFYDGDSTPCQKTAFAFGAGLLPPLYSILVIFGFGVGNMLVLLIMQHRRLQSTSIY 72
 QY 81 LNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGFIFFILLIDRY 139
 Db 73 LENLAVSLVFLFTLPFWIDYKLDWIEGDAMCKLLSGYILGLYSEIFFILLIDRY 132
 QY 140 LAIVHAFALKARTVFGVTSVITWLVAFASVPGIIFTKCKEDSVVYVCGPYFP--- 195
 Db 133 LAIVHAFALRARTVTLGIITSIITWALAILASMPALYFFKAQWETHRTCSPEFYKSL 192
 QY 196 RGNWHTIMRNILGLVPLLLIMVICYSIGILKTLRCRNEKKRHRVAVRIFTIMIVYFLF 255
 Db 193 KQWRFQALKNLGLLILPLLVMIICYAGIIRILLR-RESEKKVAVRIFAITLLFLL 251
 QY 256 WTPYNNIVILLNTFQEFFGLSNCESISOLDQATQVITLGMTCCINPITIAFVGEKFRY 315
 Db 252 WTPYNNLVSVFSAFDVLTNCEQSKHLDLQWQVTEVIATHTCCVNPILYVFGREWKY 311
 QY 316 LSVFRKHITRKFCQCPVYFRETVDGV--TSTNTPTSTGQEVSA 359
 Db 312 LRQFQRHVAVPLAKWLPLF---SVDQLERTSSISPSTGHEHLSAG 354

RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N:Alternate names: C-C CKR-3

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C:Accession: G02436; A57237

R:Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A:Reference number: H01272

A:Accession: G02436
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <PON>
 A:Cross-references: EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
 R:Combiadere, C.; Ahuja, S.K.; Murphy, P.M.
 J. Biol. Chem. 270, 16491-16494, 1995
 A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor

A:Reference number: A57237; MUID:95348056; PMID:7622448

A:Accession: A57237

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>

A:Cross-references: GB:U28694; NID:gl1199579; PIDN:AAC50469.1; PID:gl1199580

A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504

C:Genetics:

A:Gene: GDB:CMKBR3

A:Cross-references: GDB:579624; OMIM:601268

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p

F:36-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-129/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-261/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 50.1%; Score 951; DB 2; Length 355;

Best Local Similarity 52.6%; Pred. No. 2.1e-73;

Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;

QY 21 TTFEDYDYGAPCHKEDVKQIGAOQLPPLYSILVIFGFGVGNMLVLLINCKKLCLTDIY 80

Db 14 TSYID-DVGLCEKADRALMAQFPPLYSILVFTGLGNGVVMILIKYRLRIMTY 72

QY 81 LNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGFIFFILLIDRY 139

Db 73 LNLAISDLLFLITLPLFWIYVGRHNVWFGHGMCKLLSGFYHTGLYSEIFFILLIDRY 132

QY 140 LAIVHAFALKARTVFGVTSVITWLVAFASVPGIIFTKCKEDSVVYVCGPYFP--- 196

Db 133 LAIVHAFALRARTVFGVTSVITWGLAVLAALPEFIFETEELCSALYPEDTV 192

QY 197 -GWNEHTIMRNILGLVPLLLIMVICYSIGILKTLRCRNEKKRHRVAVRIFTIMIVYFLF 255

Db 193 YSWRHFHRLMTIFCLVPLLVMAICYGIITLRCPS-KKKYRAIRLIFVIMVFFIF 251

QY 256 WTPYNNIVILLNTFQEFFGLSNCESISOLDQATQVITLGMTCCINPITIAFVGEKFRY 315

Db 252 WTPYNNVAILLSSYQILFGNDCERTKHLDLVLMVTEVIATSHCCMNPVIYAEVGERKY 311

QY 316 LSVFRKHITRKFCQCPVYFRETVDGVTSNTPTSTGQEV 357

Db 312 LRHFFHRLMLHGLRYIFLPSEKLER-TSSVSPSTAEPLS 352

RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: JC4587

R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.

Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines

A:Reference number: JC4587; MUID:96136324; PMID:8573157

A:Accession: JC4587

A:Molecule type: mRNA

A:Residues: 1-360 <HOO>

A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:

A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.8%; Score 871; DB 2; Length 360;
Best Local Similarity 47.5%; Pred. No. 1.4e-66;
Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;

QY 10 IRNTNESGEVTFEDYD-YGAPCHKFDVKQGAQLLPPLYSILVIFGVGNMLVVLILI 68

Db 6 VTDQTQDETIVNSYFSEMPKPKCTKEGKAFGEVLPPLYSILVIFGVGNMLVVLVLF 65

QY 69 NCKLKCLTDIYLLNLAISDLLFTLPLWAHSAANEVFGNAMCKLFTGLVHIGYEGGI 128

Db 66 KYRKLKSWTDVYLLNLAISDLLFVLSLFPWGYAADOVWGLGCLCKIVSWMLVGVSGI 125

QY 129 FFIILLTDIYLAIVHAFVFAKARTVFGVVTSTVITWLVAVFASVPGIIFTRCKQEDSVY 188

Db 126 FFIMLSIDRYLAIVHAFVFAKARTVFGVVTSTVITWLVAVFASVPGIIFTRCKQEDSVY 185

QY 189 VCGPYF---PRGWNHFTIMRNILGLVPLIMVICYSGLIKTLRCRNEKRRHRAVRI 245

Db 186 YCKTQYSVNSTWTKVLSLEINVLGLIPLGIMLEWYSMIITLQHCCKNEK-NRAVRMI 244

QY 246 FTIMVFLFWTPYTNIVILLNTFOFFGLSNCESTSQLDOATQVETLGMTHCCINPIIY 305

Db 245 FGVVFLGFWTPYTNIVILLNTFOFFGLSNCESTSQLDOATQVETLGMTHCCINPIIY 304

QY 306 AFVGEKFRYLSVFFRKHITKR---FCQKCPVYFRETVDGVTSTNTPTSTGEQE 355

Db 305 FFLGEKFRYITQLFR---TCRGLPLVCKHCDQLQVYSDMSSSVYQSTVDHD 355

RESULT 9
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A:Note: source clone K5-5
C:Genetics:

A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.4%; Score 862.5; DB 2; Length 360;
Best Local Similarity 48.7%; Pred. No. 7.2e-66;
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

QY 31 PCHEFDVKQGAQLLPPLYSILVIFGVGNMLVVLINCKKLCGLTDIYLLNLAISDLL 90

Db 28 PCKEGIKRAGELPPLYSILVIFGVGNMLVVLINCKKLCGLTDIYLLNLAISDLL 87

QY 91 FLITPLWAHSAANEVFGNAMCKLFTGLYHIGYEGGIFFIILLTIDRYLAIVHAFVFAK 150

Db 88 FVPSLPGWYAAADQWVGLGCKMISWMLVGVSGIIFVYVLMISDRYLAIVHAFVSLR 147

QY 151 ARTVTFGVVTSTVITWLVAVFASVPGIIFTRCKQEDSVYVCGPYFPRG---WNNHFTIMRN 207

Db 148 ARTLYGVITSLATWSAVFASLPGFLFSTCYTERTNHTYCKTKYSLNSTTKVLSLEIN 207

QY 208 ILGLVPLIMVICYSGLIKTLRCRNEKRRHRAVRIFTIMVYFLFWTPYTNIVILLNT 267

Db 208 ILGLVPLIMVICYSGLIKTLRCRNEKRRHRAVRIFTIMVYFLFWTPYTNIVILLNT 266

QY 268 FQEFFGLSNCESTSQLDOATQVETLGMTHCCINPIIYAFVGEKFRYLSVFFRKHITKR 327

Db 267 LVELEVLDQCTFEYLDYAIQATETLAFVHCCNLNPIIYFFLGEKFRKYILQLEK---TCR 323

QY 328 ----FCQKCPVYFRETVDGVTSTNTPTSTGEQEVSAAGL 360

Db 324 GLFVLCQVGLLQIYSADTPSSSVYQSTMDHDLHAL 360

RESULT 10
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S55594
R:Teiford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55594
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;
Best Local Similarity 47.9%; Pred. No. 1.9e-62;
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

QY 4 TSSRFRTRNTNESCSEEVTFEFDYD---CAPCHKFDVKQGAQLLPPLYSILVIFGVGNM 61

Db 32 TTTASLPVSTNSSEYDDDDVDVEESAPCYKSTTRIAAQVFPALYLLVFLGLLGN 91

QY 62 LVVLINCKKLCGLTDIYLLNLAISDLLFTLPLWAH---SAAANEVFGNAMCKLFTGL 119

Db 92 LVVIIVIRYMKIKNLNMLNLAISDLLFTLPLFWMHYIGMYHDWTFGSLCKLLRGV 151

QY 120 YHIGYFGIIFILLTIDRYLAIVHAFVFAKARTVFGVVTSTVITWLVAVFASVPGIIFT 179

Db 152 CYMSLSYQVFCIILLTDVRYLAVYAVTALFRFTVTCGIVTCVCTWFLAGLSLPEFFPH 211

QY 180 CKCKEDSVYVCGPYF---RGWNNHFTIMRNILGLVPLIMVICYSGLIKTLRCRNE 235

Db 212 GHODNGRVQCDPYPEPMSTNVWRRAHVAKVIMLSLILPLLIMAVYVIRRLUR-RPS 270

QY 236 KKRHRAVRIFTIMVYFLFWTPYTNIVILLNTFOFFGLSNCESTSQLDOATQVETLGM 295

Db 271 KKKYKAIRLIFVINAVFVFWTPYTNIVILLNTFFHATLNLQCALSSNLDMLLITKTWAY 330


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Db      126  DRYLAIVLAANSNNNTVGHGVTSISGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE 181
QY      197  GWNNEFTIMRNI-----LGLVPLLIIMVICYSGLIKTLTLRCNEKKRHRVAVRIFTIMIVY 252
Db      182  VLQEIWPVLRNVETNFGFLPLLIINSYCFRIQTILFSCKNHKKA-KAIKILLVIVVF 240
QY      253  FLEWTYINIVILLNTQEFEGLSNCESTSQLDOATQVTTGLMTHGCCINPIYAFVGEKFK 312
Db      241  FLEWTYINMIFLETLLKLYDFPSCDMRKDLRLALSVTETVAFSHCCPLNIYAFAGERK 300
QY      313  RRYLSVFEERK 322
Db      301  RRYLYHLYGK 310

RESULT 15
JC5942
chemokine receptor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5942
R:Pan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor.
A:Reference number: JC5942; MUID:98139902; PMID:9473515
A:Accession: JC5942
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <FAN>
A:Cross-references: GB:U97123; NID:92897070; PIDN:AAC39595.1; PID:G2897071
C:Superfamily: vertebrate rhodopsin

Query Match      34.2%;      Score 649.5;  DB 2;  Length 344;
Best Local Similarity 43.0%;  Pred. No. 8.9e-48;
Matches 128;  Conservative 54;  Mismatches 99;  Indels 17;  Gaps

QY      27  DYGAPCHKFDVKVKGIGAGLLPPLYSLVYIFGFGVGNMLVLLINCKLTKGLTIDYLLANLAI 86
Db      23  DEAEQCDKYDAQAQSLAQVPSLCSAVFVIGVDNLNLLVLLVYKGLKRVENIYLLNLAV 82
QY      87  SLLFLITLPLMAHSAANWVFGNAMCKLFTGLYHLYGFGGIFIIILLTIDRYLZAIHV-A 145
Db      83  SNLCFLTLTPFWAHAG-----GDPNCKILIGLYFVGLYSETFFNCLLTQVRYLVFLHKG 136
QY      146  VFALKARTYTFGVVTSVITWLVAVFASVPGIIFTKQKEDSVYVCG-----PYPRG---W 198
Db      137  NFFSARRRVPCCIITSVLAVMTAILATLPEYVVYKPFQMEDQKYKCAFSRTFPFLPADETF 196
QY      199  NNPFITMRNTILGLVPLLIIMVICYSGLIKTLTLRCNEKKRHRVAVRIFTIMIVYFLFWTP 258
Db      197  KHELTLMKNISLVLPFLFTFFLYVQMRKTL-----RFEQRYSLFKLVFALMVVFLMWAP 253
QY      259  YNIVILLNTQEFEGLSNCESTSQLDOATQVTTGLMTHGCCINPIYAFVGEKFRRL 316
Db      254  YNIAFLSYTFKEHFSLSDCSSYNLDKSVHITKLTATTHCCINPLLYAFIDGFSKYL 311

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Best Local Similarity 46.2%; Pred. No. 5.7e-54;		
Matches 160;	Conservative 46;	Mismatches 121; Indels 19; Gaps 8;
QY	24 FQYDYG-A-PCHRFVDKQIGAQILLPPLYSLVFIFGFGVGNMLVLLINCKKLKCLTDIYLL 82	
Db	13 FEYDSDAEACYLGDIVAFGTIFLSIFYSLVFFGLVGNLLVVALTNSRKSISITDIYLL 72	
QY	83 NLAISDLLFLITLPWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIFFILITIDRYLAI 142	
Db	73 NLALSDDLLEATLPFWTHYLISHGELHNAAMCKLTATFAFFIGFGGFIFFITVISIDRYLAI 132	
QY	143 VHAFAALKARTVTFGVVTSYITWLVAVFASPGIIFETKCKEDSVYVCGPYPRGWNNEH 202	
Db	133 VLAANSMMNRKTVOHGVTIISLGVNAAAILVASPQFMETK-RKDN-----CLGDYPEVLQEIW 188	
QY	203 TLMR-----NILGLVPLLLMTWCYSGLTKTLRLCRNKKRRRAVRVIFTIMIVYFFLFWTP 258	
Db	189 PVLNRSEVNLGFVPLLLIMSCYCFRIVRTLSCNKRKA-RAIRLILLVVVFFLFWTP 247	
QY	259 YNIVILLNTFQBEFFGLSNCESTSQLDAQTVTETLGMTHCCINPIIYAFVGEKFRYLSV 318	
Db	248 YNIVIFLETLFVFNFPSCGMKRDRLWALSVTETVAFSHCCLNPFYAFAGEKFRYLRH 307	
QY	319 FFRKHLTKRFGKQCPVF-----YRETVDGVTSWTNPTSGEOEVS 357	
Db	308 LYNKCLAV-LCGR-PVHAGFSTESQRSQSDLSLTLHYTSEGEVS 351	
RESULT 14		
JC4304	orphan G protein-coupled receptor - human	
	N:Alternate names: V28 protein	
	C:Species: Homo sapiens (man)	
	C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000	
	C:Accession: JC4304	
	R:R:Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.	
	Gene 163, 295-299, 1995	
	A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g	
	A:Reference number: JC4304; MUID:96011651; PMID:7590284	
	A:Accession: JC4304	
	A:Molecule type: mRNA	
	A:Residues: 1-355 <RAP>	
	A:Cross-references: GB:U20350; NID:9665580; PIDN:AAA91783.1; PID:9665581	
	A:Experimental source: peripheral blood mononuclear cell	
	C:Comment: This protein is a cell-surface receptor which recognizes extracellular signals	
	C:Comment: This protein is a key regulator of many immune and homeostatic responses, and	
	C:Genetics:	
	A:Gene: v28	
	A:Map position: 3pter-p21	
	C:Superfamily: vertebrate rhodopsin	
	C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein	
	F:35-57/Domain: transmembrane #status predicted <TM1>	
	F:66-88/Domain: transmembrane #status predicted <TM2>	
	F:104-125/Domain: transmembrane #status predicted <TM3>	
	F:146-165/Domain: transmembrane #status predicted <TM4>	
	F:197-217/Domain: transmembrane #status predicted <TM5>	
	F:230-254/Domain: transmembrane #status predicted <TM6>	
	F:275-296/Domain: transmembrane #status predicted <TM7>	
Query Match	37.3%;	Score 708; DB 2; Length 355;
Best Local Similarity	46.8%;	Pred. No. 9.8e-53;
Matches 145;	Conservative 47;	Mismatches 108; Indels 10; Gaps 5;
QY	18 EEWTFEDY-DYCAPCHKFDVKQIGAQILLPPLYSLVFIFGFGVGNMLVLLINCKKLKCL 76	
Db	6 ESVTEFEDYDLAEACYIGDIVVFGVIVFISIFYSIFAIGLVGNLLVVALTNSRKPVS 65	
QY	77 TDYLLNLAISDLLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGFIFFILLTI 136	
Db	66 TDYLLNLAISDLLFLVATLPFWTHYLINKEGLHNAAMCKLTATFAFFIGFGSIFFIIVISI 125	
QY	137 DRYLATVHAIVFAALKARTVTFGVVTSYITWLVAVFASPGIIFETKCKEDSVYVCGPYPR 196	

